

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Frameshift Weight:	0		

Quality:	928	Length:	865
Ratio:	3.916	Gaps:	1
Percent Similarity:	99.578	Percent Identity:	99.578

```
Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      . = 1
```

DD0017Rsid62 x BB1410sid8 July 2, 2007 15:28 .

50 atggcggccaatcgggcgcggtgagcgggaggaggcagcggcagcgg 99  
1 MetAlaAlaAsnAlaGlyGlyGlyGlyAlaGlyGlySerGlySerGl 17  
100 cagcgtggctgcgcggcggtgtgcgccccagcggctcgcggtggacgc 149  
18 ySerValAlaAlaProAlaValCysArgProSerGlySerArgTrpThrP 34  
150 cgacgcccggagcagatcaggatgctgtaaggagctctactacggtgcggc 199  
35 roThrProGluGlnIleArgMetLeuLysGluLeuTyrTyrGlyCysGly 50  
200 atccggtcgccccagctcgagcagatccagcgcataccgcgcattgctgcg 249  
51 lleArgSerProSerSerGluGlnIleGlnArgIleThrAlaMetLeuAr 67

```

250 gcagcacggcaagatcgagggaagaacgtcttctactggttccagaacc 299
   |||||||||||||||||||||||||||||||||||||||||||||||
68 gGlnHisGlyLysIleGluGlyLysAsnValPheTyrTrpPheGlnAsnH 84
   |||||||||||||||||||||||||||||||||||||||||||||||
300 acaagggcccgagcgccagaagcgccgctcaccagcctcgacgtcaac 349
   |||||||||||||||||||||||||||||||||||||||||||||||
85 isLysAlaArgGluArgGlnLysArgArgLeuThrSerLeuAspValAsn 100
   |||||||||||||||||||||||||||||||||||||||||||||||
350 gtgcccggcgccggcgccgacgcccaccaccagccaactcggcgctcct 399
   |||||||||||||||||||||||||||||||||||||||||||||||
101 ValProAlaAlaGlyAlaAlaAspAlaThrThrSerGlnLeuGlyValLe 117
   |||||||||||||||||||||||||||||||||||||||||||||||
400 ctgcgtgtcgtcgccgcccgttcaggtagctgcgtcagtgctgtggtg 449
   |||||||||||||||||||||||||||||||||||||||||||||||
118 uSerLeuSerSerProProPro..... 124
      .
      .
      .
550 ctgatgtgcaccgtcgtcatcactgatcaggcgccgcccctccctcgccc 599
      |||||||||||||||||||||||||||||||||||||||||||
125 .....SerGlyAlaAlaProProSerPro 132
      .
      .
600 accctcggcttctacgccgcccgaatggcgccggatcggctgtgctgct 649
   |||||||||||||||||||||||||||||||||||||||||||||||
133 ThrLeuGlyPheTyrAlaAlaGlyAsnGlyGlyGlySerAlaValLeuLe 149
   |||||||||||||||||||||||||||||||||||||||||||||||
650 ggacacgagttccgactggggcagcagcgccgctgccatggccaccgaga 699
   |||||||||||||||||||||||||||||||||||||||||||||||
150 uAspThrSerSerAspTrpGlySerSerGlyAlaAlaMetAlaThrGluT 166
   |||||||||||||||||||||||||||||||||||||||||||||||
700 catgcttctcgcaggtcgggtcgtgtagtagcttctttcttgggcattgc 749
   |||||||||||||||||||||||||||||||||||||||||||||||
167 hrCysPheLeuGlnValGlyAlaValValArgSerPheLeuGlyHisCys 182
   |||||||||||||||||||||||||||||||||||||||||||||||
750 gcgcagttttcacgttcgtacgtacgagttgatcgccgcgtcgttccatcc 799
   |||||||||||||||||||||||||||||||||||||||||||||||
183 AlaGlnPheHisValArgThrTyrGluLeuIleAlaAlaSerPheHisPr 199
   |||||||||||||||||||||||||||||||||||||||||||||||
800 accggtatatataactgttaggtacggcggtgcccgcgccgaggactaca 849
   |||||||||||||||||||||||||||||||||||||||||||||||
200 oProValTyrIleThrValArgTyrGlyGlyAlaArgProGlnAspTyrM 216
   |||||||||||||||||||||||||||||||||||||||||||||||
850 tggcgctgacggacacgggcagctcgtcgcagtgccacgcttctcgtcg 899
   |||||||||||||||||||||||||||||||||||||||||||||||
217 etGlyValThrAspThrGlySerSerSerGlnTrpProArgPheAlaSer 232
   |||||||||||||||||||||||||||||||||||||||||||||||
900 tcggacacgataatg 914
   |||||||||||||||
233 SerAspThrIleMet 237

```

**FrameAlign** of: DD0017Rsid62 check: 2905 from: 1 to: 1638

Genomic DNA from 3DT corresponding to p0016.ctsas50r, US 10/744,572

to: DD0017sid6 check: 2251 from: 1 to: 237

SEQ ID NO: 6 is encoded by EST sequence of p0016.ctsas50r

Scoring matrix: blosum62.cmp

CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Translation table: transl\_table\_01.txt transl\_table = 1

This file contains the Standard Code specified in the feature table definition, Version 1.08, formatted for use with the GCG programs (Data Files volume of the Data Reference Set). It names amino acids in both one and three-letter form and lists the codons which should translate into them. All GCG translation programs may generate their . .

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Frameshift Weight:	0		

Quality:	929	Length:	868
Ratio:	3.903	Gaps:	1
Percent Similarity:	99.580	Percent Identity:	99.580

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 2
. = 1
```

DD0017Rsid62 x BB1410SID6 August 5, 2007 14:09 ..

```

      .      .      .      .      .      .      .      .      .      .
50 atggcgcccaatgcgggcggcggtggagcggaggaggcagcggcagcg 99
|||||
1 MetAlaAlaAsnAlaGlyGlyGlyGlyAlaGlyGlyGlySerGlySerG1 17

100 cagcgtggctgcgcggcggtgtgccgccccagcggctcgcggtggagc 149
|||||
18 ySerValAlaAlaProAlaValCysArgProSerGlySerArgTrpThrP 34

150 cgacgcccggagcagatcaggatgctgaaggagctctactacggctgcgc 199
|||||
35 roThrProGluGlnIleArgMetLeuLysGluLeuTyrTyrGlyCysGly 50

200 atccggtcgccagctcggagcagatccagcgcacaccgccatgctgcg 249
|||||

```

```

51 IleArgSerProSerSerGluGlnIleGlnArgIleThrAlaMetLeuAr 67

250 gcagcacggcaagatcgagggcaagaacgtcttctactggttcagaacc 299
|||||
68 gGlnHisGlyLysIleGluGlyLysAsnValPheTyrTrpPheGlnAsnH 84

300 acaagcccgagcgccaggaagcgccgctcaccagcctcgacgtcaac 349
|||||
85 isLysAlaArgGluArgGlnLysArgArgLeuThrSerLeuAspValAsn 100
|||||
350 gtgcccgccgcccgcgcggcgacgcaccaccagccaactcggcgctct 399
|||||
101 ValProAlaAlaGlyAlaAlaAspAlaThrThrSerGlnLeuGlyValLe 117

400 ctgcgtgtcgtcgccgccccttcaggtacgtgcgtcagtgctgtggtg 449
|||||
118 uSerLeuSerSerProProPro..... 124
.
.
.

550 ctgatgtgcaccgctcgtcatcactgatcaggcgccgcccctccctgcgcc 599
|||||
125 .....SerGlyAlaAlaProProSerPro 132

600 accctcggttctacgccgcggcaatggcgccggatcggtgtgctgct 649
|||||
133 ThrLeuGlyLeuTyrAlaAlaGlyAsnGlyGlyGlySerAlaValLeuLe 149

650 ggacacgagttccgactggggcagcagcgccgctgccatggccaccgaga 699
|||||
150 uAspThrSerSerAspTrpGlySerSerGlyAlaAlaMetAlaThrGluT 166

700 catgcttcctgcaggtcgggtgctgtagtacgttctttcttgggcattgc 749
|||||
167 hrCysPheLeuGlnValGlyAlaValValArgSerPheLeuGlyHisCys 182

750 gcgagtttcacgttcgtacgtacgagttgatcgcccgctcgttccatcc 799
|||||
183 AlaGlnPheHisValArgThrTyrGluLeuIleAlaAlaSerPheHisPr 199

800 accggtatatataactgttaggtacggcggtgcgcgcccgcaggactaca 849
|||||
200 oProValTyrIleThrValArgTyrGlyGlyAlaArgProGlnAspTyrM 216

850 tggcgctgacggacacgggcagctcgtcgcagtggccacgcttctcgtcg 899
|||||
217 etGlyValThrAspThrGlySerSerSerGlnTrpProArgPheSerSer 232

900 tcggacacgataatggcg 917
|||||
233 SerAspThrIleMetAla 238

```